PATENT COOPERATION TREATY

PCT

INTERNATIONAL PRELIMINARY EXAMINATION REPORT

(PCT Article 36 and Rule 70)

Applicant's or agent's file reference 21044-33-1PC	**FOR FURTHER ACTION**	See Notification of Transmittal of International Preliminary Examination Report (Form PCT/IPEA/416)
International application No. PCT/US03/11867	International filing date *(day/month/year)* 15 April 2003 (15.04.2003)	Priority date *(day/month/year)* 15 April 2002 (15.04.2002)
International Patent Classification (IPC) or national classification and IPC IPC(7): C12Q 1/68 and US Cl.: 435/6		
Applicant RIGEL PHARMACEUTICALS, INC.		

1. This international preliminary examination report has been prepared by this International Preliminary Examining Authority and is transmitted to the applicant according to Article 36.

2. This REPORT consists of a total of 6 sheets, including this cover sheet.

   ☒ This report is also accompanied by ANNEXES, i.e., sheets of the description, claims and/or drawings which have been amended and are the basis for this report and/or sheets containing rectifications made before this Authority (see Rule 70.16 and Section 607 of the Administrative Instructions under the PCT).

   These annexes consist of a total of 9 sheets.

3. This report contains indications relating to the following items:

   - I ☒ Basis of the report
   - II ☐ Priority
   - III ☒ Non-establishment of report with regard to novelty, inventive step and industrial applicability
   - IV ☒ Lack of unity of invention
   - V ☒ Reasoned statement under Article 35(2) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement
   - VI ☐ Certain documents cited
   - VII ☐ Certain defects in the international application
   - VIII ☐ Certain observations on the international application

Date of submission of the demand	Date of completion of this report
14 November 2003 (14.11.2003)	21 May 2004 (21.05.2004)
Name and mailing address of the IPEA/US Mail Stop PCT, Attn: IPEA/US Commissioner for Patents P.O. Box 1450 Alexandria, Virginia 22313-1450 Facsimile No. (703) 872-9306	Authorized officer Sheela S. Huff Valerie Bell-Harrison Telephone No. (571) 272-1600

Form PCT/IPEA/409 (cover sheet)(July 1998)

INTERNATIONAL PRE[redacted]NARY EXAMINATION REPORT

International application No.
PCT/US0[redacted]57

I. Basis of the report

1. With regard to the **elements** of the international application:*

☒ the international application as originally filed.

☒ the description:
pages 1-5,10-13,15-60.62-76,78 as originally filed
pages 6-9a,14,61,77, filed with the demand
pages NONE, filed with the letter of _____.

☒ the claims:
pages 79-83, as originally filed
pages NONE, as amended (together with any statement) under Article 19
pages NONE, filed with the demand
pages NONE, filed with the letter of _____.

☒ the drawings:
pages 1-63, as originally filed
pages NONE, filed with the demand
pages NONE, filed with the letter of _____.

☒ the sequence listing part of the description:
pages 1-54, as originally filed
pages NONE, filed with the demand
pages NONE, filed with the letter of _____.

2. With regard to the **language**, all the elements marked above were available or furnished to this Authority in the language in which the international application was filed, unless otherwise indicated under this item.
These elements were available or furnished to this Authority in the following language _____ which is:

☐ the language of a translation furnished for the purposes of international search (under Rule23.1(b)).

☐ the language of publication of the international application (under Rule 48.3(b)).

☐ the language of the translation furnished for the purposes of international preliminary examination(under Rules 55.2 and/or 55.3).

3. With regard to any **nucleotide and/or amino acid sequence** disclosed in the international application, the international preliminary examination was carried out on the basis of the sequence listing:

☒ contained in the international application in printed form.

☒ filed together with the international application in computer readable form.

☐ furnished subsequently to this Authority in written form.

☐ furnished subsequently to this Authority in computer readable form.

☐ The statement that the subsequently furnished written sequence listing does not go beyond the disclosure in the international application as filed has been furnished.

☐ The statement that the information recorded in computer readable form is identical to the written sequence listing has been furnished.

4. ☒ The amendments have resulted in the cancellation of:

☒ the description, pages none

☒ the claims, Nos. none

☒ the drawings, sheets/~~fig~~ none

5. ☐ This report has been established as if (some of) the amendments had not been made, since they have been considered to go beyond the disclosure as filed, as indicated in the Supplemental Box (Rule 70.2(c)).**

** Replacement sheets which have been furnished to the receiving Office in response to an invitation under Article 14 are referred to in this report as "originally filed" and are not annexed to this report since they do not contain amendments (Rules 70.16 and 70.17).*

*** Any replacement sheet containing such amendments must be referred to under item 1 and annexed to this report.*

INTERNATIONAL PRE[redacted]NARY EXAMINATION REPORT

International application No.
PCT/US03/[redacted]867

III. Non-establishment of opinion with regard to novelty, inventive step and industrial applicability

1. The question whether the claimed invention appears to be novel, to involve an inventive step (to be non-obvious), or to be industrially applicable have not been and will not be examined in respect of:

☐ the entire international application,

☒ claims Nos. 23-35 and 1-22 as they read on proteins other than BAP-1

because:

☐ the said international application, or the said claim Nos. ____ relate to the following subject matter which does not require international preliminary examination *(specify)*:

☐ the description, claims or drawings *(indicate particular elements below)* or said claims Nos. ____ are so unclear that no meaningful opinion could be formed *(specify)*:

☐ the claims, or said claims Nos. ____ are so inadequately supported by the description that no meaningful opinion could be formed.

☒ no international search report has been established for said claims Nos. 23-35 and 1-22 as they read on proteins other than BAP-1

2. A meaningful international preliminary examination cannot be carried out due to the failure of the nucleotide and/or amino acid sequence listing to comply with the standard provided for in Annex C of the Administrative Instructions:

☐ the written form has not been furnished or does not comply with the standard.

☐ the computer readable form has not been furnished or does not comply with the standard.

INTERNATIONAL PRE[redacted]NARY EXAMINATION REPORT

International [redacted]plication No.
PCT/US03/[redacted]867

IV. Lack of unity of invention

1. In response to the invitation to restrict or pay additional fees the applicant has:
   - ☐ restricted the claims.
   - ☐ paid additional fees.
   - ☐ paid additional fees under protest.
   - ☐ neither restricted nor paid additional fees.

2. ☒ This Authority found that the requirement of unity of invention is not complied with and chose, according to Rule 68.1, not to invite the applicant to restrict or pay additional fees.

3. This Authority considers that the requirement of unity of invention is accordance with Rules 13.1, 13.2 and 13.3 is
   - ☐ complied with.
   - ☒ not complied with for the following reasons:

(See continuation sheet)

4. Consequently, the following parts of the international application were the subject of international preliminary examination in establishing this report:
   - ☐ all parts.
   - ☒ the parts relating to claims Nos. 1-22 as they read on BAP-1

INTERNATIONAL PRE[redacted]NARY EXAMINATION REPORT

Internatio[redacted]plication No.
PCT/US0[redacted]67

V. Reasoned statement under Rule 66.2(a)(ii) with regard to novelty, inventive step or industrial applicability; citations and explanations supporting such statement

1. STATEMENT

Novelty (N)	Claims	1-22 as they read on BAP-1	YES
	Claims	NONE	NO
Inventive Step (IS)	Claims	1-22 are they read on BAP-1	YES
	Claims	NONE	NO
Industrial Applicability (IA)	Claims	1-22 as they read on BAP-1	YES
	Claims	NONE	NO

2. CITATIONS AND EXPLANATIONS

Claims 1-22 (as they read on BAP-1) meet the criteria set out in PCT Article 33(2)-(3), because the prior art does not teach or fairly suggest the claimed invention.

Claims 1-22 (as they read on BAP-1) the criteria set out in PCT Article 33(4), and thus the industrial applicability because the subject matter claimed can be made or used in industry.

---------- NEW CITATIONS ----------

Supplemental Box
(To be used when the space in any of the preceding boxes is not sufficient)

IV. 3. This Authority considers that the requirement of unity of invention is accordance with Rules 13.1, 13.2 and 13.3 is not complied with for the following reasons:
This application contains the following inventions or groups of inventions which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I, claim(s) 1-22, drawn to a method of identifying a compound that modulates cell cycle arrest and determining the chemical or phenotypic effect of the compound.

Group II, claim(s) 23, drawn to a method for identifying a compound that modulates cell cycle arrest and determining the physical effect of the compound prior to determining the chemical or phenotypic effect.

Group III, claim(s) 24-33, drawn to modulating cell cycle arrest in a subject by administering the compound identified by Group I.

Group IV, claim(s) 34, drawn to modulating cell cycle arrest by administering a target polypeptide.

Group V, claim(s) 35, drawn to modulating cell cycle arrest by administering a nucleic acid which encodes a target polypeptide.

In addition, with Group 1, applicant will have BAP-1 examined without paying additional fees.
In addition, if applicant pays for Group II, they will get Group II as they read on BAP-1. If applicant wants any more proteins, then they need to pay additional fees.
In addition, if applicant pays for Group III, they will get Group III as they read on BAP-1. If applicant wants any more proteins, then they need to pay additional fees.
In addition, if applicant pays for Group IV, they will get Group IV as they read on BAP-1. If applicant wants any more proteins, then they need to pay additional fees.
In addition, if applicant pays for Group V, they will get Group V as they read on BAP-1. If applicant wants any more proteins, then they need to pay additional fees.

The inventions listed as Groups I-V do not relate to a single general inventive concept under PCT Rule 13.1 because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Each of the methods of Groups I-V require the use of different products and require different steps. Each of the products in Groups I-V differ structurally and functionally and thus lack the same corresponding technical feature..

According to PCT Rule 13.2 and to the guidelines in Section (f)I)(B)(1) of Annex B of the PCT Administrative Instructions, all alternatives of a Markush Group must have a common structure, which is a significant structural element. Although the polypeptides listed in the claims share a common structure of a single amino acid, the compounds are not regarded as being of similar nature because the shared common structure is not a significant element. A common structure of a single amino acid is not a significant structural element because the amino acid is found in every peptide or protein.

threonine kinase 15 (ARK2), transmembrane 4 superfamily member 1, or ERCC1 polypeptide may be encoded by a nucleic acid that hybridizes under stringent conditions to a nucleic acid encoding a polypeptide having an amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, or 28.

A further embodiment of the invention provides a method of modulating cell cycle arrest in a subject. A therapeutically effective amount of a BRCA-1-Associated Protein-1 (BAP-1), Nuclear Protein 95 (NP95), Fanconi anemia group A protein (FANCA), DEAD/H box polypeptide 9 (DDX9), insulin-like growth factor 1 receptor (IGF1R), ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1), aldehyde dehydrogenase, pyruvate kinase, glucose-6-phosphate dehydrogenase, HCDR-3, DEAD/H box polypeptide 21 (DDX21), serine threonine kinase 15 (ARK2), transmembrane 4 superfamily member 1, or ERCC1 polypeptide is administered to the subject. The BRCA-1-Associated Protein-1 (BAP-1), Nuclear Protein 95 (NP95), Fanconi anemia group A protein (FANCA), DEAD/H box polypeptide 9 (DDX9), insulin-like growth factor 1 receptor (IGF1R), ubiquitin-conjugating enzyme E2 variant 1 (UBE2V1), aldehyde dehydrogenase, pyruvate kinase, glucose-6-phosphate dehydrogenase, HCDR-3, DEAD/H box polypeptide 21 (DDX21), serine threonine kinase 15 (ARK2), transmembrane 4 superfamily member 1, or ERCC1 polypeptide may be encoded by a nucleic acid that hybridizes under stringent conditions to a nucleic acid encoding a polypeptide having an amino acid sequence of SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, or 28.

Other embodiments and advantages of the present invention will be apparent from the detailed description that follows.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 provides a nucleotide (SEQ ID NO:1) and amino acid sequence (SEQ ID NO:2) of human BAP-1.

Figure 2 provides an illustration of the relevant domains of BAP-1, including the ubiquitin hydrolase domain and the DNA binding domain. Also shown is the BAP-1 functional hit (G3-2D8; SEQ ID NOS:36 and 37) isolated in the retroviral screen. The functional hit is in the antisense orientation BstXI linkers = SEQ ID NOS:38 and 39.

Figure 3 illustrates cell tracker assay data demonstrating that GFP-fused BAP-1 is antiproliferative in A549 cells. The BAP-1 construct is the functional hit isolated in the retroviral screen. Figure 3 top left illustrates fluorescence analysis of green fluorescent protein (GFP) infected A549.tTA control cells. Figure 3 top right illustrates cell tracker assay

data from GFP infected A549.tTA control cells. Figure 3 lower left illustrates fluorescence analysis of BAP-1 infected A549.tTA cells. Figure 3 lower right illustrates cell tracker assay date from BAP-1 infected A549.tTA cells.

Figure 4 provides a nucleotide (SEQ ID NO:3) and amino acid sequence (SEQ ID NO:4) of human NP95.

Figure 5 provides an illustration of the relevant domains of NP95, including the ubiquitin like domain, the zinc finger domain, the nuclear protein domain, and the ubiquitin ligase domain G1-2635 = SEQ ID NO:40.

Figure 6 illustrates cell tracker assay data demonstrating that GFP-fused NP95 is antiproliferative in A549. The NP-95 construct is the functional hit isolated in the retroviral screen. Figure 6 top left illustrates fluorescence analysis of green fluorescent protein (GFP) infected A549.tTA control cells. Figure 6 top right illustrates cell tracker assay data from GFP infected A549.tTA control cells. Figure 6 lower left illustrates fluorescence analysis of NP95 infected A549.tTA cells. Figure 6 lower right illustrates cell tracker assay date from NP95 infected A549.tTA cells.

Figure 7 provides a nucleotide (SEQ ID NO:5) and amino acid (SEQ ID NO:6) sequence of human FANCA.

Figure 8 provides a nucleotide (SEQ ID NO:7) and an amino acid (SEQ ID NO:8) sequence of human DDX9. DEAD (Asp-Glu-Ala-Asp) box motif = SEQ ID NO:60.

Figure 9 provides a nucleotide (SEQ ID NO:9) and an amino acid (SEQ ID NO:10) sequence of human IGF1R.

Figure 10 provides a nucleotide (SEQ ID NO:11) and an amino acid (SEQ ID NO:12) sequence of human UBE2V1.

Figure 11 provides a nucleotide (SEQ ID NO:13) and an amino acid (SEQ ID NO:14) sequence of human aldehyde dehydrogenase.

Figure 12 provides a nucleotide (SEQ ID NO:15) and an amino acid (SEQ ID NO:16) sequence of human pyruvate kinase.

Figure 13 provides a nucleotide (SEQ ID NO:17) and an amino acid (SEQ ID NO:18) sequence of human G6PD.

Figure 14 provides a nucleotide (SEQ ID NO:19) and an amino acid (SEQ ID NO:20) sequence of human HCDR-3.

Figure 15 provides a nucleotide (SEQ ID NO:21) and an amino acid (SEQ ID NO:22) sequence of human DDX21.

Figure 16 provides a nucleotide (SEQ ID NO:23) and an amino acid (SEQ ID NO:24) sequence of human ARK2.

Figure 17 provides a nucleotide (SEQ ID NO:25) and an amino acid (SEQ ID NO:26) sequence of human transmembrane 4 superfamily member 1.

Figure 18 provides a nucleotide (SEQ ID NO:27) and an amino acid (SEQ ID NO:28) sequence of human ERCC1.

Figure 19 provides an illustration of certain relevant domains of FANCA, including the aldehyde dehydrogenase cysteine active site, FKBP-type peptidyl-prolyl cis-trans isomerase signature 1 site, the PX site, and the peptidase S8 site. G2-2F3 = SEQ ID NO:41.

Figure 20 illustrates cell tracker assay data demonstrating that GFP-fused FANCA is antiproliferative in A549 cancer cells. The FANCA construct is the functional hit isolated in the retroviral screen. Figure 20 top left illustrates fluorescence analysis of green fluorescent protein (GFP) infected A549.tTA control cells. Figure 20 top right illustrates cell tracker assay data from GFP infected A549.tTA control cells. Figure 20 lower left illustrates fluorescence analysis of FANCA infected A549.tTA cells. Figure 20 lower right illustrates cell tracker assay date from FANCA infected A549.tTA cells.

Figure 21 provides an illustration of certain relevant domains of DDX9, including the double stranded RNA binding motif, the DEAD/H box helicase domain, the helicase conserved C terminal domain, and the CLN3 protein domain. G3-2H6 = SEQ ID NOS:42 and 43; BstXI linkers = SEQ ID NOS:38 and 39; DEAD box = SEQ ID NO:60.

Figure 22 illustrates cell tracker assay data demonstrating that GFP-fused DDX9 is antiproliferative in A549 cancer cells. The DDX9 construct is the functional hit isolated in the retroviral screen. Figure 22 top left illustrates fluorescence analysis of green fluorescent protein (GFP) infected A549.tTA control cells. Figure 22 top right illustrates cell tracker assay data from GFP infected A549.tTA control cells. Figure 22 lower left illustrates fluorescence analysis of DDX9 infected A549.tTA cells. Figure 22 lower right illustrates cell tracker assay date from DDX9 infected A549.tTA cells.

Figure 23 provides an illustration of certain relevant domains of IGF1R, including the receptor L domain, the furin-like cysteine rich region, the fibronectin type II domain, the transmembrane domain, and the kinase domain. G3-2H2_1 = SEQ ID NO:44.

Figure 24 illustrates cell tracker assay data demonstrating that GFP-fused IGF1R is antiproliferative in A549. The IGF1R construct is the functional hit isolated in the retroviral screen. Figure 24 top left illustrates fluorescence analysis of green fluorescent

protein (GFP) infected A549.tTA control cells. Figure 24 top right illustrates cell tracker assay data from GFP infected A549.tTA control cells. Figure 24lower left illustrates

fluorescence analysis of IGF1R infected A549.tTA cells. Figure 24 lower right illustrates cell tracker assay date from IGF1R infected A549.tTA cells.

Figure 25 provides an illustration of the relevant domains of UBE2V1, including the ubiquitin conjugating enzyme domain. G3-2G2/2H2 = SEQ ID NOS:45 and 46; BstXI linkers = SEQ ID NOS:38 and 39.

Figure 26 illustrates cell tracker assay data demonstrating that GFP-fused UBE2V1 is antiproliferative in A549 cancer cells. The UBE2V1 construct is the functional hit isolated in the retroviral screen. Figure 26 top left illustrates fluorescence analysis of green fluorescent protein (GFP) infected A549.tTA control cells. Figure 26 top right illustrates cell tracker assay data from GFP infected A549.tTA control cells. Figure 26 lower left illustrates fluorescence analysis of UBE2V1 infected A549.tTA cells. Figure 26 top right illustrates cell tracker assay date from UBE2V1 infected A549.tTA cells.

Figure 27 shows portions of G3_2H2 (SEQ ID NOS:47 and 54) and portions of four alternatively spliced UBE2V1 transcripts (SEQ ID NOS:48-53, 55 and 56).

Figure 28 provides some cDNA sequence isolated from a cell tracker assay for cDNAs that regulate the cell cycle, *i.e.,* functional hits from the retroviral screen (SEQ ID NOS:29-35).

Figure 29 provides Uch-l3 (SEQ ID NO:57) and dominant negative mutants of BAP-1 (SEQ ID NO:58). Mutated residues are shown with arrows.

Figure 30 provides evidence that expression of Bap1 WT and protease mutants is antiproliferative in HeLa cells.

Figure 31 provides evidence tthat expression of Bap1 WT protein is antiproliferative in HeLa cells in the Celltracker assay.

Figure 32 provides evidence that expression of Bap1 protease mutants is slightly more antiproliferative than expression of Bap1 WT in H1299 cells.

Figure 33 provides evidence expression of Bap1 WT and Bap1 protease mutants is antiproliferative in H1299 cells in the Celltracker assay.

Figure 34 provides evidence that the Bap1 functional hit G32D8 is antiproliferative in HMEC cells.

Figure 35 provides evidence that the Bap1 functional hit G3-2D8 is antiproliferative in PrEC cells.

Figure 36 provides evidence that BAP1 specific siRNA has an antiproliferative effect on HeLa cells.

Figure 37 provides evidence that BAP1 specific siRNA induces G1 arrest in H1299 cells.

Figure 38 provides evidence that soluble GST-Bap1 protein can be expressed from SF9 cells. GST-Bap1 was produced using the baculovirus transfer vector pDEST20

Imamura, *et al., Nuc. Acids Res.* 26(9):2063 (1998); and Zhang *et al., J. Cell. Sci.* 112:2693 (1999)). Vectors containing DNA encoding DDX9 complement yeast that have mutations in *prp8-1*, the yeast homolog of DDX9 (*see* Imamura *et al.*). Helicase assays known to those of skill in the art can be used, e.g., to identify modulators of DDX9.

IGF1R encodes a cell surface tyrosine kinase receptor and binds to IGF1 ligand (*see, e.g.,* Nakae *et al., Endocr. Rev.* 22(6):818 (2001); Flier *et al., Proc. Nat'l Acad. Sci. USA* 83:664-668 (1086); Francke *et al., Cold Spring Harb. Symp. Quant. Biol.* 51(Pt. 2):855-866 (1986); Ullrich *et al., EMBO J.* 5:2503-2512 (1986); Cooke *et al., Biochem. Biophys. Res. Commun.* 177:1113-1120 (1991); Abbott *et al., J. Biol. Chem.* 267:10759-10763 (1992); Werner *et al., Proc. Nat'l Acad. Sci. USA* 93:318-8323 (1996); Grant *et al., J. Clin. Endocrinol. Metab.* 83:3252-3257 (1998); and Butler & LeRoith, *Endocrinology* 142(5):1685 (2001)). Upon ligand binding, the receptor undergoes a conformational change which enables it to bind ATP, thereby increasing their kinase activity and modulate cell proliferation (*see* Nakae *et al.*). IGF1R deficient mice develop cell proliferation disorders, including muscle hypoplasia due to decreased cell numbers; IGF1R null mice develop cell proliferation disorders including dwarfism (*Id.*). Overexpression of IGF1R has been linked to increased radioresistance of breast cancer cells (*see* Macaulay *et al., Oncogene* 22(6):4029 (2001)). Ligand binding assays, autophosphorylation assays, kinase assays, and signal transduction assays known to those of skill in the art can be used, e.g., to identify modulators of IGF1R.

UBE2V1 encodes a protein that has been show to play a role in cell cycle regulation (*see, e.g.*, Rothofsky *et al., Gene* 195:141-149 (1997); Sancho *et al., Mol. Cell. Biol.* 18:576-589 (1998); Ma *et al., Oncogene* 17:1321-1326 (1998); Hofmann & Pickart, *Cell* 96:645-653 (1999); Deng *et al., Cell* 103:351-361 (2000); and Thomson *et al., Genome Res.* 10:1743-1756 (2000)). Constitutive expression of exogenous UBE2V1 inhibits the capacity of colorectal adenocarcinoma cells to differentiate upon confluence and inhibits the mitotic kinase cdk1, thereby inducing the cells to arrest at the G_2-M phase of the cell cycle (*see,* Sancho *et al., Mol. Cell. Biol.* 18(1):576 (1998) and Stubbs *et al., Am. J. Path.* 154(5):1335 (1999)). UBE2V1 has four alternatively spliced transcripts that encode proteins with the conserved Ubc domain of E2 enzymes and unique N-terminal sequence (see Figure 27). Ubiquitination assays, e.g., ubiquitin ligase assays, known to those of skill in the art, can be used to identify modulators of UBE2V1.

Aldehyde dehydrogenases form a superfamily of NADP+ dependent enzymes that are involved in several distinct metabolic pathways (*see* Vasilou *et al., Chem. Biol.*

Synthetic polymers, such as polyurethanes, polyesters, polycarbonates, polyureas, polyamides, polyethyleneimines, polyarylene sulfides, polysiloxanes, polyimides, and polyacetates can also form an appropriate tag or tag binder. Many other tag/tag binder pairs are also useful in assay systems described herein, as would be apparent to one of skill upon review of this disclosure.

Common linkers such as peptides, polyethers, and the like can also serve as tags, and include polypeptide sequences, such as poly Gly sequences of between about 5 and 200 amino acids (SEQ ID NO:59). Such flexible linkers are known to persons of skill in the art. For example, poly(ethylene glycol) linkers are available from Shearwater Polymers, Inc. Huntsville, Alabama. These linkers optionally have amide linkages, sulfhydryl linkages, or heterofunctional linkages.

Tag binders are fixed to solid substrates using any of a variety of methods currently available. Solid substrates are commonly derivatized or functionalized by exposing all or a portion of the substrate to a chemical reagent which fixes a chemical group to the surface which is reactive with a portion of the tag binder. For example, groups which are suitable for attachment to a longer chain portion would include amines, hydroxyl, thiol, and carboxyl groups. Aminoalkylsilanes and hydroxyalkylsilanes can be used to functionalize a variety of surfaces, such as glass surfaces. The construction of such solid phase biopolymer arrays is well described in the literature. *See, e.g.*, Merrifield, *J. Am. Chem. Soc.* 85:2149-2154 (1963) (describing solid phase synthesis of, e.g., peptides); Geysen *et al., J. Immun. Meth.* 102:259-274 (1987) (describing synthesis of solid phase components on pins); Frank & Doring, *Tetrahedron* 44:60316040 (1988) (describing synthesis of various peptide sequences on cellulose disks); Fodor *et al., Science*, 251:767-777 (1991); Sheldon *et al., Clinical Chemistry* 39(4):718-719 (1993); and Kozal *et al., Nature Medicine* 2(7):753759 (1996) (all describing arrays of biopolymers fixed to solid substrates). Non-chemical approaches for fixing tag binders to substrates include other common methods, such as heat, cross-linking by UV radiation, and the like.

IMMUNOLOGICAL DETECTION OF BAP-1, NP95, FANCA, DDX9, IGF1R, UBE2V1, ALDEHYDE DEHYDROGENASE, PYRUVATE KINASE, G6PD, HCDR-3, DDX21, ARK2, TRANSMEMBRANE 4 SUPERFAMILY MEMBER 1, OR ERCC1 POLYPEPTIDES

In addition to the detection of BAP-1, NP95, FANCA, DDX9, IGF1R, UBE2V1, aldehyde dehydrogenase, pyruvate kinase, G6PD, HCDR-3, DDX21, ARK2,

Example 12: BAP-1 WT protein, protease mutants, siRNA and antisense functional hit are antiproliferative.

The BAP-1 functional hit identified in the retroviral screen is in the antisense orientation. (Figure 2). Expression of the functional hit in a tumor cell line, *e.g.*, A549 cells, or in untransformed cells, *e.g.*, HMEC or PrEc cells, was antiproliferative. (See, *e.g.*, Figures 3, and 34-35.)

Dominant negative mutants of BAP-1 were made by mutating residues in the protease domain. (See, *e.g.*, Figure 29.) Using two different assays, expression of BAP-1 wild-type and protease mutants was antiproliferative in tumor cell lines, *i.e.*, HeLa cells and H1299 cells. (See, *e.g.*, Figures 30-33). siRNA molecules derived from the BAP-1 nucleic aicd were shown to be antiproiferative in HeLa cells and H1299 cells. (See, *e.g.*, Figures 36-37.)

Example 13: BAP-1 is a ubiquitin protease.

GST-Bap-1 was expressed in and purified from SF9 cells. (See, *e.g.*, Figures 38-39.) Using a fluorogenic ubiuquiting cleavage assay, BAP-1 was shown to be an active ubiquitin protease, with a Km of 0.5 μM for the substrate UbAMC. (See, *e.g.*, Figures 40-42.) UbCHO was also demonstrated to be a specific inhibitor of BAP-1. (See, *e.g.*, Figure 43.)

Assays for ubiquitin hydrolase activity (*e.g.*, to assay BAP-1 activity) can also be performed as described in U.S. Patent No. 6,307,035 and Mayer and Wilkinson, *Biochemistry* 28:166(1989) using the glycine 76 ethyl ester of ubiquitin as a substrate. Peak areas can be integrated and normalized with respect to the ubiquitin standard.

Example 14: NP95 WT protein, ring finger mutants, siRNA and functional hit are antiproliferative.

The NP95 (G1-2635) functional hit (G1-2635) identified in the retroviral screen is in the sense orientation. (Figure 5). Expression of the functional hit in a tumor cell line, *e.g.*, A549 cells, or in untransformed cells, *e.g.*, HMEC or PrEc cells, was antiproliferative. (See, *e.g.*, Figures 6, and 44-45.) siRNA molecules derived from the NP-95 nucleic acid were shown to be antiproiferative in PrEc and HUVEC cells and H1299 cells. (See, *e.g.*, Figures 46-47, and 57.)

Using real time PCR analysis, NP95 mRNA expression was shown to be overexpressed in tumor tissue relative to normal tissue from the same patient. Increased